

# FIGURE 1

APPROVED	O.G. FIG.	SUBCLASS
	CLASS	
BY		DRAFTSMAN

GGACTAATCTGTGGAGCAGTTATTCCAGTATCACCCAGGGTGAGCCACACCAGGACTGT  
GTTGAAGGGT TTTTTCTTTAAATGTAATACCTCCTCATCTTTCTTACACAGTG  
TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA  
CTACTCTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCTGGTTGTGCTCTGCCAACCCCTCTTAGCCCTCACACATCGCACT  
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAAGCCATTTTCCA  
TTTGATCTGTTCCAATGTGTCATTGGATGTCAGTGCTATTACGAGTTGTACATTGTC  
AGATTTAGGTTGACCTCAGTCCCACCAACATTCCATTGATACTCGAATGCTGATCTC  
AAAACAATAAAATTAAAGGAATCAAAGAAAATGATTTAAAGGACTCACTTACATTG  
CTGATCCTGAACAAACAAGCTAACGAAGATTCAACCCAAAAGCCTTCTAACCAAAAGAA  
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAAGTGAATACCACTTAATCTCCCAAAT  
CATTAGCAGAACTCAGAATTGAAATAAGTTAAGAAAATACAAAAGGACACATTCAA  
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTCTGATAATAATGGGATAGA  
GCCAGGGGCATTGAAAGGGTGACGGTGTCCATATCAGAATTGCGAGCAGAAAAGTGCAC  
CAGTCCCTAAAGGCTTACCAACTTATTGGAGCTCACTTAGATTATAATAAAATTCA  
ACAGTGGAACTTGAGGATTAAACGATAACAAAGAACTACAAAGGCTGGGCTAGGAAACAA  
CAAAATCACAGATATGAAAATGGGAGTCTGCTAACATACCACTGAGAGAAAATACATT  
TGGAAAACAATAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCCAGATA  
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTCTGCTCAAACAGTG  
AAAGATGAAGAAATCTTATACAGTGCAATAAGTTATTCAACAAACCCGGTGAATACTGG  
AAATGCAACCTGCAACATTGTTGTGTTGAGCAGAATGAGTGTTCAGCTGGAACTTT  
GGAATGTAATAATTAGTAATTGGTAATGTCATTAAATATAAGATTCAAAATCCCTACATT  
TGGAAATACTGAACTCTTAATAATGGTAGTATTATATAACAGCAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACCGAATTGCGAAACTATT  
GATACATAAGGGTTGAGAGAAACAAGCATCTATTGCGAGTTCTTGTGCGTACAAATGAT  
CTTACATAAAATCTCATGCTTGACCATTCCTTCTCATAACAAAAAGTAAGATATTGGTA  
TTAACACTTGTATCAAGCACATTAAAGAACTGTACTGTAATGGAATGCTTGACT  
TAGCAAAATTGCTCTTCATTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTATTCTTAGTAACTGGTAGTACTGTAATATTAAAT  
CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCGT  
CTTATGTTAAAACAATTCTTAAAGCCTCAGTAAATGTTCTTACCAACTGA  
TAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTAATTATT  
ACCTGATTAAAAATCTCTGAAAAACGTGAGTGTTCATAAAATCTGTAACTCGCATT  
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTTGAGATATCCCTTGGAGACCTGCTGGAGAGCCTGG  
CACTAACAAATTCTACACCAAATTGCTCTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA  
TATAATGCTCAGAGTTCTTATGTATTCTTATTGGCATTCAACATATGTAATCAGAAA  
ACAGGGAAATTTCATTAAAAATATTGGTTGAAAT

FOTS 80-2984-1650

## **FIGURE 2**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392  
<subunit 1 of 1, 379 aa, 1 stop  
<MW: 43302, pI: 7.30, NX(S/T): 1  
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDSLFPTRREPR  
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ  
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI PRVREIHLENNKLKKIPSGLPEL  
KYLQIIFLHSNSIARVGVNDFCPTVPKMKSLSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

**Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBC ASS

PROTEIN ID: 238111650

# FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCGSGCACCGCCCCGGCCCTCCGCCCTCCGCACTCGGCCTCC  
CTCCCTCCGCCGCTCCCGCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC  
GGCCCCGCCGGCCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTGCCCTCCGGCCGGCCGGCGCCGGCCAGA  
GCCCGGGCTGCTGCCCATCCGTTCTGAGAAAGGAGCCGCTGCCGTTGGGAGCGGCAGGCTGCACCTCGCAG  
GAAGGTCTATGCCTTGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTGGGGTGTGCTGCGCTGCTGTG  
CGCCTGCGAGGCGCCTCAGTGGGTGCCGTACCAGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACAGA  
GTGCCCAACCCGGCCTGTGGCAGCCGCCAGCTGCCGGACACTGCTGCCAGACCTGCCAGGAGCGCAG  
CAGTTGGAGCGGCAGCCGAGGCCCTGTCCTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTAGCGACCG  
CGGGGAGCCAGGCCCTGAGGAGCGGGCCGTGGTACGCCACACGGACTTCGTGGCCTGCTGACAGGGCCGAG  
GTCGCAGGCCGTGGCACGAGCCGAGTCTGCTGCCCTAGGCCCTCGCTCTATCTCCTACAGGGGGCT  
GGACGCCCTACCAGGATCCGCTCTCAGACTCCAATGGCAGTGTCCCTGTTGAGCACCCCTGCAGCCCCACCA  
AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGTTGTCTGCGGCTCCTTAGGGCAGAACAGCTGCA  
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGAGGTCTGGGGCCTCTCATCCGCACCAGGGCCCTGGCTGC  
AGAGACCTTCAGTCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCTAGGGGCATCACCTGCTCAGTCT  
CAGTGACACAGAGGACTCCTGCATTGGCTCTCAGACTCCAATGGCAGTGTCCCTGTTGAGCACCCCTGCAGG  
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACATTCAAGGCAATGTCTCAG  
GGAACCAGGCTTGCTGAGGTCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGCTGGGAGCTGCA  
GATGGCCCTGGAGTGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT  
CCTGCAAAGTGTCTTGCTGGGCTGATGCCCTGATCCCAGTCCAGACGGGTGCTGCCGCTCAGCCAGCCTCAC  
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGCTGCCATGAC  
GGAGACCAAGCCTCAGCGGAGGGATCAGCGACTGCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC  
GGCGTGGGTATCTGCCCTGGCTGGTGCCGAGGGCTCATATGCTGCTGAGAATGAGCTCTCCTGAACGT  
GGGCACCAAGGACTTCCAGACGGAGAGCTCGGGGGCACGTGGCTGCCCTGCCCCTACTGTGGCATAAGGCC  
CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC  
CTGGCTTCCTGGATAACCACTGTCACCTGCACTATGAAGTGTCTGGCTGGCTGGCTCAGAACAG  
CACTGTCACTGCCAACCTCTGGCCTCCTGGAACGCCAGGGCTCGCGGCTGCTGAAGGGATTCTATGGCTC  
AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCGGAACCTGCTGCCACCTGGCAAAAGGCATGCCCTCCCTGAT  
GATCACCAAGGGTAGCCCCAGAGGGAGCTCGAGGGCAGGTGACATAGCCAACCAATGTGAGGTTGGCG  
ACTGCGCTGGAGCGCCGGGGCCAGGGGCTGGCTGGCTGCCACCCGGTGCAGGCTCC  
TGTGGCCTGGTCTCCGCCCTAGGCCGCCAACCTGGTGGCTGGGCCAGGGGGCTCCGGATACAGCTCTGCTGCC  
CTTCTCGAGGGCAGCGGCCAACGGGCTCGCTGGCGCCAACTACGACCCGCTCTGCTCACTCTGCAC  
CTGCCAGAGACGAACGGTGTGACCCGGTGTGACCCGGTGTGCCCCACGGCCAGCTGCCACACCCGGTGCAGGCTCC  
CGACCAAGTGTGCCCTGTTGCCCTGAGAAACAAGATGTCAGAGACTTGCCAGGGCTGCCAAGGAGCCGGACCC  
AGGAGAGGGCTGCTATTTGATGGTAGCCGGAGCTGGCGGGCAGCGGGTACCGGGTGGCACCCGGTGTGCC  
CTTGGCTTAATTAAGTGTGTCTGCACCTGCAAGGGGGCAGTGGAGAGGTGCACTGTGAGAAGGTGAGTG  
TCCCCGGCTGGCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGCTGG  
GGCCCAACCCAGCTGGGGACCCCATGCAGGCTGATGGGCCCGGGCTGCCGTTTGCTGGCAGTGGTCCC  
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCTTTGGAGAGATGAGCTGTATCACCTGAGATGTGGGAG  
GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCCTGTGGCTGGGGAGAGAGTCAGTGTGTT  
CCGCTGCACGGCCACCGGGCCCCAGAGACCAAGTCAAGGAGCTGGAGAAAGAACAGCCGAAGGCTCTTA  
GGGAGCAGCCAGAGGGCAAGTGACCAAGAGGATGGGCCAGCTGGGAAGGGTGGCATCGAGGACCTTCTT  
GCATTCTCCTGTGGGAAGCCCAGTGCCTTTGCTCCTCTGTCCTGCCCTACTCCCACCCCACTACCTCTGGAA  
CCACAGCTCCACAAGGGGAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCCCTGCCCTGCCACCC  
TCGGCCTCTGTCTGGAGGCCAACCCCTTCCCTGTACATAATGTCACTGGCTGGTGGGATTTAATT  
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG  
TTTGTATTAAAACATTCTTCAAGTCAAAAAAAAAAAAAA

O.G. FIG.	SUBCLASS
CLASS	
BY DRAFTSMAN	

TO 780-29844166

## FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pi: 8.21, NX(S/T): 5

O.G. FIG.	SUBCLASS
APPROVED	CLASS
BY DRAFTSMAN	

MPSLPAPPAPLLLGLLLGSRPARGAGPEPPVLPIRSEKEPLPVRGAAGCTFGGKVYALDE  
TWHPDLGQPFGVMRVCVLCAEAPQWGRRTGPGRVSKNIKPECPTPACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVAR  
ARVSLLRSSLRFSISYRRLDRPTRIRFSDNSGVLFEHPAAPTQDGLVCGVWRAPRLSLRL  
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTQEMD  
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLSQVLCGADALIPVQTGAAGSASLTLLGN  
GSЛИYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVTAAHLLGPPGTPGPRLLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTGSPRGELRGQVHIANQCEVGLRLEAAGAEGVRALGAPDTASAAPPV  
PGLPALAPAKPGGPGPRDPNTCFEGQQRPHGARWAPNYDPLCLSLCTCQRRTVICDPVVCP  
PPSCPHPVQAPDQCCPVCPEKQDVRDLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPPVVPFF  
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCKQCPVGSAGHPQLGDPMQADG  
PRGCRCFAGQWFPEQSWHPSVPPFGEMSCI TCRCGAGVPHCERDDCSLPLSCGSGKESRCCS  
RCTAHRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

## FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTTCGCAGCTCGTCGCCACTGCCACCGCCGCCGTCACTGCG  
TCCGGCTCCGGCTCCGCCCTCCGGCCGGCCATGCAGCCCCGCCGCCAGGCGCCGGTGCAGCTGC  
TGCCCGCGCTGGCCCTGCTGCTGCTCGAGCGGGGCCAGGGCAGCTCCCTGGCCAACC CGGTGCCCG  
CCGCGCCCTTGTCTGCCCCGGCGCAGCCCTGCCGAATGGGGGTGTGCACTCGCAGCCCTG  
AGCGGACCCGCAGCACCCGCCCGCCGGCAGCCTGGCTACAGCTGCACCTGCCCGGGATCTCGGCG  
CCAAGTGCCAGCTTGTGAGATCCTTGCCAGCAACCTTGTACCATGGCAACTGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCAATTGCAATGAAGGCTATGAAGGCTCCAACTGTGAACAGGCAC  
TCCCAGCCA CTGGCTGGACCGAATCCATGGCACCCGACAGCTCAGCCTGTTCTGCTACTCAGGAGCCTGACA  
AAATCTGCCTCGCTCAGCAACGGTACACTGCCAACCTGGCAGCCAAAACAGGGAGAAAGTTGAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCTGTGGGAATGCCAGTTCAACAGCTCTGCCGGTGGCC  
GCCGGTATCCTTGAAGTGCCACAGAACACCTCAGTCAGTAAGATTGCCAGATGCCACTGCCACTGATTG  
TCTGGAAAGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT  
CAGGGGACTGGTCTCCTGGAGGAGATGCTGCCCTGGGAATAACTTATTGGTTTGTGAATGATTCTG  
TGACTAAGTCTATTGGCTTGCCTTAACCTGGTGGTAAGGTCAGCACCGTCAAGGGCAACTTTCTGTACCTGTG  
CAAATGACTGGAGTGGTACTTCTGGAAGAATACGATGCTGCCAGAGGAACCTGCCAAAACAACGCGAGCT  
AGGAGCAGTACGTGGTACTTCTGGAAGAATACGATGGAGCAATTACCTGTGTTGCCCTGGTTACTGGAGAGCTT  
GTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTTGCCCTGGTTACTGGAGAGCTT  
GCCAGTCCAAGATTGATTACTGCATCCAGACCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATACTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCCCTCGCTCTCGT  
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCCAGCCCCGGCTTCACAGGGCGA  
CCTGTGCCAGCTATTGACTTCTGCCCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGCACCGACT  
ACAAATGCCCTGTGATCCAGGTACCATGGCCTACTGTGAGGAGGAATAATGAGTGCCTCCGCTCCAT  
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTCCTGGCAGAATACAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCCTAACGTCAGCTGTCTGAACGGAGCACCTGTGACAGGACGGCTGA  
ATGGCACGTGCATCTGTGCAACCGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC  
CCTGCCACCATGGTGGAGCTGCCCTGGACCAGCCAATGGCTATGAGTGTGTCCTGGCAGAATGCCACGGCACTCCC  
CAAACGTGAGATCCACCTCAATGGAAGTCCGGCACATGGCGAGAGCCTCACCAACATGCCACGGCACTCCC  
TCTACATCATCATTGGAGCCTCTCGTGGCCTCATCCTTATGCTGATCATCTGATCGTGGGATTGCCGCA  
TCAGCCGATTGAATACCAGGGTTCTCCAGGCCAGCCTATGAGGAGTTCTACAACTGCCGAGCAGCG  
AGTTCAAGCAATGCCATTGCATCCATCCGGATGCCAGGTTGGAAAGAAATCCGGCTGCAATGTATGATGTGA  
GCCCATGCCATGAAGATTACAGTCTGATGACAACCCCTGGTACACTGATTAAACTAAAGATTGTAAT  
CTTTTTGGATTATTTCAAAAAGATGAGATACTACACTCATTAAATTTAAGAAAATAAAAGCTTAA  
GAAATTAAAATGCTAGCTCAAGAGTTTCAGTAGAAATTTAAGAACTAATTCTGAGCTTTAGTTG  
GAAAAATATTTAAAACAAAATTGTGAAACCTATAGACGATTTAATGTACCTCAGCTCTAAACTGT  
GTGCTTCTACTAGTGTGCTTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTGGTTGTACA  
GAATAAGTCTAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCCTTCTGAGTAGAGTTAGGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATAACCGTTACTTAAAAGAAGTCTGAAATGTTGTTGTGGAAA  
AGAAACTAGTTAAATTACTATTCCAACCGAATGAAATTAGCCTTGCCTTATTCTGTCATGGTAAGTAAC  
TTATTCTGCACTGTTGTAACCTTGTGAAACATTCTTCAGGTTTTGTCATTTCGTAACAGTCG  
TCGAACTAGGCCCAAAAACATACGTAACGAAAAGGCCAGCGAGGCAAATTCTGATTGATTGAATCTATATT  
TTCTTAAAAGTCAGGGTTCTATATTGTGAGTAATTAAATTACATTGAGTTGTTGCTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTTCCTCAGTAGTGAGTATTCTCATAGTGCACTTATTATCTCCAGGATGTT  
TTTGTGGCTGTATTGATATGTGCTTCTGATTCTGCTAATTCCAACCATATTGAATAATGTGATC  
AAGTCA

O.G. FIG.	SUBCLASS
APPROVED	CLASS
BY	
DRAFTSMAN	

1984-11-06 0

## **FIGURE 6**

>subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, PI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALLLLLLGGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNNGVCTSR  
PEPDHQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHHGNCSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKEIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC  
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG  
YHGLYCEEYNECLSAAPCLNAATCRDLVNGYEJVCLAEYKGTHCELYKDPCANVSCLNGATC  
DSDGLNGTCIAPGFTGEECIDINECDSNPCHHGSCLDQPNGYNCHCPHGWGANCEIHL  
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN  
CRSIDSEFSNIAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

### Signal sequence.

## amino acids 1-28

#### Transmembrane domain.

### amino acids 641-660

#### N-glycosylation sites.

N-glycosylation, amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365, 375-379, 442-446, 549-553, 564-568

#### Glycosaminoglycan attachment site.

amino acids 320-324

#### Threonine kinase phosphorylation sites.

amino acids 490-498, 674-682

#### **Uninoculation sites.**

N-myristoylation sites:  
amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

### Amidation site.

amino acids 702-706

aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

all domain-cysteine pattern signatures.

**EGF-like domain cysteine pattern signature:**  
amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## FIGURE 7

CTCTGGAAGGTACGGCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC  
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTACCTGTGTTGCCTTCC  
TGGTTACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

APPROVED	O.G. FIG.
CLASS	SUBCLASS
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"FIGURE 7" 2941-1650

## **FIGURE 8**

CTCTGGAAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC  
CTGGTGGTGAAGGTACGACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACACGAAGCCGTACAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTGCCTTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	
DRAFTSMAN	

100-303101-2-2000-00000

## FIGURE 9

GCTGAGTCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACC**ATGCCGGGCACCTAC**  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCTGCAAGAGCAGGCACGGCCCT  
GATGCAGGGACTTCCCCTCGTGACGGCCACAACGACCTGCCCTGGTCTAAGGCAGGTTT  
ACCAGAAAGGGTACAGGATGTTAACCTGCGCAATTCTAGCTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCCTCATCGGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA  
GCTCCGCTAAGGGGTCCACTCCTCTACAACAAACATCAGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTCTCCACTCGCTGCC  
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGA  
TTGGTGGAGATTATGATGGGCCGGCAAATTCCCTCAGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCT  
TCGTGGAAACCTGCTGCGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCTGGAGGACAAGTTCCGGATGAGCAGCTGAGCAGTTCCCTGCCACTCCGACCTC  
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTGAGATTCCCATACA  
CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG  
TCCTGCAAGTTGTGGCCACCTTCCCAGTCCTTATTCTGTGGCT**CTGA**TGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA  
AATATTCTGAAATAATGTTTGGACATAG

O.G. FIG.	SUBCLASS
APPROVED	CLASS
BY	DRAFTSMAN

100E80-29441660

## FIGURE 10

APPROVED	O.G. FIG.	SUBCLASS
BY	DRAFTSMAN	

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLACLIGVEGGHSDLNSLSILRTFYMLGVRYLTLCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDSLHVSDAVARALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGG DYDGAGKF P QGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEKWQS PLEDKFPD EQLSSS
CHSDL SRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPVLILWL
```

**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

PROTEIN: 2E9-11660

## FIGURE 11

AAAACCTATAATATTCCGGATTATTCATACCGTCCCACCATGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTGACCACACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCTGATGCGGGACTTCCGCTCGTGGACGGCCAC  
AACGACCTGCCCTGGTCCTAAGGCAGGTTACCAAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTCAGCTACGCCAGACCAGCCTGGACAGGCTTAGAGATGCCCTCGTGGCGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACGGGATGCCCTGCCCTCACCTGGAG  
CAGATTGACCTCATGCCGCATGTGTGCCTCCATTCTGAGCTGGAGCTGTGACCTCGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTACGGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGGTCCACTCCTCTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGCAGAAATGAACCGCCTGGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGTGTGCAACAGTGCTCGGAATGTTCC  
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTGTGATGGTGTCTTGTCCATGG  
GAGTAATACAGTGCACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTCGACCACATC  
AAGGCTGTCATTGGATCCAAGTTCATCGGATTGGTGGAGATTATGATGGGCCGGCAAATT  
CCCTCAGGGCTGGAAGACGTGTCCACATACCGGTCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCCGGTCTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCTGGAGGACAAGTTCCGGATGA  
GCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACTCACTGAGATTCCCACACTGGACAGCCAAGTTACCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCACCCTGACAAAACACATGCCACCCTGCCAGCACCTGA  
ACTCCTGGGGGACCGTCAGTCTCCTTCCCCAAAACCCAAGGACACC

APPROVED	O.G. FIG.	SUBCLASS
BY	CLASS	DRAFTSMAN

107580-298441650

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872  
><subunit 1 of 1, 446 aa, 0 stop  
><NX(S/T): 5  
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVVAEMNRLGMMVDSLHVSDAVARALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGG DYDGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQS PLEDKFPDEQLSSS  
CHSDLRQSLTGQELTEIPIHWTAKLPACKWSVSESSPHDKTHCPPCPAELLGGP  
SVFLFPPPKPKDT

APPROVED	O.G. FIG.	SUBCLASS
BY	CLASS	
DRAFTSMAN		

PRINTED "2008-06-16 09:44:42"

## FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGGCC  
CTGCGCCACCGCCGCCGAGCCGAGCCCCGCCGCGGCCGGCAGCGCCGCCATGCCC  
GCCGGCCGCCGGGGCCCCGCCGCCAATCCGCGGGCGCCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA  
GCTGCTGCTCTGCGTCCTCGGGGCGCCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA  
GTCCCCAGGATCCCACGCTCTCATCGGCTCCTCCCTGCTGGCACCTGCTCAGTGCACGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTACTGGACCCTAACGGGCCGCTGCC  
TGAGCTCTCCCGTGTACTCAACGCCTCACCTGGCTCTGGCCCTGGCAACCTCAATGGGT  
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGG  
TCCTGCCTCTATGTTGGCCTGCCCTGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCTCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTACCA  
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACGCCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGCCGCTGGGGCCTGGAG  
GACCAGCTGAGCGTGGCTGGTGTGCCACCCGCCCTCAAGGATTCTCTTCAAGCAA  
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA  
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTCGTGCAGTGC  
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC  
CACAGCCGCTCCACTCCCCGAGCTGGGGCCGGTGCAGCTCAAGCAGTTCTGGCTGGCTC  
GGGGCGGAGAGCCGAGCTGGGGCCGGTGCAGCTCAAGCAGTTCTGGCTGGGAT  
AAGAAGCACCGTACTGCTCCAACCTCAGCTCCGCCTACGACCAGTGGCGAGCCTGGAT  
GCAGAAGTCGCACAAGACCCGCAACCAGGACGGAGGGATCTGCCCTGGGAGACGGGCA  
CGCGAGAGGTCCAGATAGCCTGAGGGCTCAGGCCACCCCTGCCACGTGGAGA  
CGCAGAGGCCAACCAAATGCCTGAGGGCCACCTCTGTACCCCTACTCAGGGCACCTGAGCCAC  
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT  
GAGGCCACCTTGGTGCACCCAGTGGGTGTGTGTGAGGGTTGGTTGAGTTGC  
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC  
CCTCCAAAAGAGTCCTTAAATAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

O. G. FIG.	SUBCLASS
CLASS	
APPROVED	BY
DRAFTSMAN	

10100-29844-65

## FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNRRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRGSA RDVLTLDILDVVTTDPPP DVHVS RVGG  
LEDQLSVRWVSP PALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR LAGLKPGTVYFVQ  
VRCNPF GIYGSKKAGI WSEW SHPTAA STPR SERPGPGGACE PRGGE PSSGP VRREL KQFLG  
WLKKHAYCSNLSFR LYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

APPROVED	O.G. FIG.	SUBCLASS
BY	CLASS	
DRAFTSMAN		

**Signal sequence.**

amino acids 1-30

**Transmembrane domain.**

amino acids 44-61

**N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

**N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

**Amidation site.**

amino acids 3-7, 79-83, 411-415

**Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

## FIGURE 15

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGGATGGAAATTCTTCTGGACATCCTC  
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGTGCCAAGGTTACACCTTG  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAA  
GGCATTCTTCTGCAATGACGAAGAATAACCATGGCATATTGTCACTGTGGCTCGGCAG  
CTGGACATGTCTCGGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGG  
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTC  
TCTGTGTCCTAATTGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTTCTAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT  
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAAGCACCTAGTTCTGAAAATGATTACAGGTTAGGTTGATGTCATCTA  
ATAGGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA  
TCATTGGAGGCTTGGCAGTCTCATTACTACCACCTGTTAGCCAAAGCTGATT  
ACATATGATATAACAGAGAAACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTCACCTGAAGGCTTGCAA  
AATTGTACCATACCGTTATTAAACATATATTATTGATTGCACTTAAATTGTT  
ATAATTGTGTTCTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA  
TGAAGGACTATCTAGGGTATTCTACAATGAATATCATGAACCTCAATGGTAGGTT  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTAAAAAAA  
AAAAAAA  
AAAAAAA

O.G. FIG.	SUBCLASS
CLASS	
APPROVED	BY
DRAFTSMAN	

NOTE 80 " 2198414666

## FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436  
<subunit 1 of 1, 300 aa, 1 stop  
<MW: 32964, pI: 9.52, NX(S/T): 1  
MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 170-187

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

**N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

TOP SECRET 29844660

APPROVED	O. G. FIG.
BY	CLASS
DRAFSMAN	SUBCLASS

## FIGURE 17

GA~~T~~ACTTTCTTGGAGTCTGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCA  
GGGTGACGGCAGGGCAGGGGGCGCTGGCCGGGAGAAGCGC~~GGGG~~CTGGAGCACCA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCAAGGAGGCCATGGGAGCCGGAGGGGGACT  
GCGAGAGGACCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGG  
TGCTCCTGGGCTGGCGCCGGCTGCCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGGCACCCGGCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGCCG  
CGATGGCCGCGACGGCCGCGACGGCGCCGGCTCCGGAGAGAAAGGCGAGGGCGGG  
GGCCGGGACTGCCGGGACCTCGAGGGACCCGGCCGAGGAGAGGCCGGACCCGGCGGG  
CCCACCGGGCTGCCGGGAGTGCTCGGTGCCTCCGCATCCGCCCTCAGGCCAAGCGCTC  
CGAGAGCCGGGTGCCTCCGGCTTGACGCACCCCTGCCCTCGACCGCGTGTGGTAACG  
AGCAGGGACATTACGACGCCGTACCGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTAAGAATGGCGA  
ATCCATTGCCTCTTCTTCCAGTTTCTGGGGGTGGCCAAGCCAGCCTCGCTCTGGGG  
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTGCTTAGTGCCACTGCAAAGTGAGCTATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT  
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGAAC  
AGTGGCTGTGCGATCAGGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGTCTCTCCGTCTGCTCTGGATCCTCCACCCCTGCTCCTGG  
GCCGCCCTTCTCAGAGATCACTCAATAAACCTAAGAACCCCTATAAAAAAAAAAAAA  
AAAAAAAAAAAA

APPROVED	O. G. FIG.
	SUBCLASS
BY	CLASS
DRAFTSMAN	

TOP SECRET 298441560

## FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592  
><subunit 1 of 1, 243 aa, 1 stop  
><MW: 25298, pI: 6.44, NX(S/T): 0  
MRPLLVLLLLGLAAGSPLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGRPGLPGPRGDGPGRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASI KTDSTFSGFLVYSDWHSSPVFA

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	
DRAFTSMAN	

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

PROT#E301-2981-1650

## FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTCTTGTCTCCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA  
GCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCTG  
CAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTGTGAAGTGGTCAG  
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCCAGGAGAGTGTGCTCGAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAAGCCTTGTCTGTGCCTACTCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTC  
ACGGCCGGTTCCGGAGGGAGTGCTCGTGCCTGTGACATCGGCTACGGGGAGCCAG  
TGTGCCACCAAGGTGCATTTCCCTCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG  
GGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTGCCTCTATCTGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT  
CACCTACAAGACCGCCAAGGACTCCTCCGCTGGCCACAGGGAGCACCAGGCCTCACCA  
GTTTGCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTCAACTGGAACGACCAGCGCTGCAAAC  
CCGAAACCGTTACATCTGCCAGTTGCCACAGGAGCACATCTCCGGTGGGCCAGGGCCT  
GAGGCCTGACCACATGGCTCCCTGCCCTGCCCTGGGAGCACCAGGCTTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGCCAGGTTAAGACCACATGCCTCATGTCAAAGAGGTCTCAGA  
CCTTGCACAATGCCAGAAGTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTGTGATTGGAAAGATGGCTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTGGCCAGAC  
CCTGTGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAATTATGAATCAG  
CTGAAAAAAAAAAAAA

O.G. FIG.	SUBCLASS
CLASS	
APPROVED	BY
DRAFTSMAN	

1070320-1984766

## FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQQAPMAGALNRKESFLLSLHNRLRSWV  
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG  
NWEVNGKTIIPYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH  
CHCPPGYTGRYCQVRCSSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFFHTCDLRIDGDC  
FMVSSEADTYYRARMKCQRKGGLAQSQKVQDILAFYLGRLETTNEVTDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLAAAGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHISRWGPSS

**Signal sequence.**

amino acids 1-26

**Transmembrane domain.**

amino acids 110-124

**N-glycosylation sites.**

amino acids 144-148, 243-247

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 45-49

**N-myristoylation sites.**

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,

288-294, 331-337, 398-404

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 204-215

**EGF-like domain cysteine pattern signature.**

amino acids 249-261, 280-292

**C-type lectin domain signature.**

amino acids 417-442

APPROVED :	O.G. FIG.
CLASS :	SUBCLASS
BY	DRAFTSMAN

1984-08-22 08:56:50

## FIGURE 21

CGGACGCGTGGCTGGCGCTGCAAAGCGTCCCAGCGGGTCCCCGAGCGTCCCGCGCCCT  
CGCCCCGCCATGCCTGCTGCTGGGCTGTGCCTGGGCTGTCCCTGTGTGGGGTCGA  
GGAAGAGGCGCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCCAGGCAAG  
TCAGACTGTTGAGAGGCTGAAAACAAACCTTGATGACAGAATTCTCAGTGAAGTCTACC  
ATCATTCCCCTATGCCTCACTACGGTTCCAGAATGCTGAACAGAGCTTCTGAAGA  
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCAAATTACAGAGAGAGAAAAGAAGAGTGGTGTAGG  
GTAAAAGAGAAAAGGAATAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCA  
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCTTTCTGAGTTATGAGGAGCTTC  
TGCAGAGGCGCTGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCCCAGCAGCTGTCCGG  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATGCATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCAGAGGGCAGTGGCGGGGAAGATGATTCTGGCCTCCCCAT  
CTACTGTCATTAACCAAAATGAAACATTGCCAACATAATTTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTGGGACATCCAGTTCTAAATGGCTATTGTGCACTACTTGCTCCTA  
AAGACCTTCCTCCTTACCAAGAATGTGGTATTGTGCTTGACAGCAGTGCTTCTATGGTG  
GGAACCAAACCTCGGCAGACCAAGGATGCCCTTCACAATTCCATGACCTCCGACCCCA  
GGACCGTTTCAGTATGGATTTCACCGGATCAAAGTATGGAAGGACACTTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGAAAGTGTACATTACCCATATGTACCCACTGGA  
GGCACAGACATCAACGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCA  
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTCCTGACGGATGGGAAGGCCACGG  
TCGGGAGACGCACACCCCTCAAGATCCTCAACAACACCCGAGAGGCCGCCCCAGGCAAGTC  
TGCATCTTCACCATTGGCATCGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT  
GGAGAACTGTGGCCTCACCGCGCTCCTCTGACATCCGCATCGATTATCCCCCAGC  
GGTTCTACGATGAAATCAGGACCCGCTCTGACATCCGCATCGATTATCCCCCAGC  
TCAGTGGTGAGGCCACCAAGACCCCTGTTCCCAACTACTTCAACGGCTCGGAGATCATCAT  
TGCAGGAAAGCTGGTGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA  
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT  
GTCACAGGAAGCCCCAGGCCCTGGAGGGCGATGGAGAGGGGACACCAACACATCGAGCGTCT  
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTACGATGAAACGG  
AGAAGGAGCGCTGCCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACGCATGGATGGCTGGAGGAGGCCACGG  
CATGTCGGCTGCCATGGACCCGAACCGGTGGTCAGAGCGTGCAGGAGCTGGCACGCAGC  
CAGGACCTTGCTCAAGAAGCCAAACTCCGTAAAAAAACAAAACAAAACAAAAAAAGA  
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGATACGATGAGAAGATGGCCACCT  
GCAAGCCAGGAAGACGCCCTCACAGACACCATGTCTGCTGGCACCTGATCTGGACCTC  
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

APPROVED	D.G. F.C.
CLASS	SUBCLASS
BY	
DRAFTSMAN	

00944680  
101401

## FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIS  
RYAFTTVSCRMLNRASEDQDIEFQMGIPIAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE  
KRKNKTTEENGEKGTEIFRASAVIPS KDKA AFFLSYEELLQRRLGKYEH SISVRPQQLSGR LS  
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANII FKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRKVWKDHLISVTPDSIRDGKVIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTGDGKPTVGETHTLKILNNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEIIAGKL VDRKLDHLHVEVTASN SKFII LKTDVPVRPQKAGKDVTG  
SPRP GGDGE GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAH GMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKT KKRHGR  
DGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

APPROVED	C.G. FIG.
CLASS	SUBCLASS
BY CRAFTSMAN	

DRAFTSMAN'S SIGNATURE

## FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC  
GGCAGCGGCGGCCGGCGCCCTCCGGCTCCGGCTCTGCTGTTGCTCTCCGCCGCG  
CACTGATCCCCACAGGTGATGGCAGAACTGTTACGAAAGACGTGACAGTGATCGAGGG  
GAGGTTGCGACCACAGTTGCCAAGTCATAAGAGTGACGACTCTGTGATTCAAGCTACTGAA  
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGACAGCAGGTTCAAGT  
TGCTGAATTTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA  
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCCACGACTATCAGGTGGTCAA  
GGGAACACAGAGCTAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACATGGGTCCAGTGTACTGCCAGGTGG  
AGCACCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTCAAGATGACTTACCTCTACAAGGCTTAACCCGGAAAGGGACCGCTTGA  
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGCTGGGCCAACCTGTTCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCACAAACAACCACCA  
CCACCAACCACCACCAACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATGGTGGCGTGGCGGTGGTGGTGGTGGTGG  
GCTGTGCTTGCATCATTCTGGGCGCTATTGCCCCAGACATAAGGTACATACTTCACTC  
ATGAAGCCAAGGAGCCGATGACGCAGCAGACGCAGACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATTAGATCAGCCTTTGTTCAAT  
GAGGTGTCCAACTGGCCCTATTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVFAMLCLLIIILGRYFARHKGYFTHEAKGADDAADADTAIINAEGGQNSEE
KKEYFI
```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
	DRAFTSMAN	

### Signal sequence.

amino acids 1-36

#### Transmembrane domain.

amino acids 372-393

### N-glycosylation sites.

N-glycosylation at amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310, 430-434

#### Tyrosine kinase phosphorylation sites.

inc. acids 233-240, 319-328

#### N-nitrosylation sites.

N-myristoylation sites:  
amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

## FIGURE 25

O.G. FIG.	SUBCLASS
APPROVED	CLASS
BY DRAFTSMAN	

FOTEC 80 - 29341660

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTGGGCCGA  
CCCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGCTCCCTGCGCCGCCGCCCT  
CCGGGACAGAAGATGTGCTCCAGGGCTCCCTGCTGCTGCCGCTGCTACTGGCCCT  
GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGAGCCACAGACAGTCTTCT  
GCACTGCCGCCAGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC  
GTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCTGCCGGCTGCA  
GCTCTGGACCTGTCACAGAACAGATGCCAGCCTGCCCTGCCCCGCTGCTGCTGG  
ACCTCAGCCACAACAGCCTCTGGCCCTGGAGGCCGGCATCCTGACACTGCCAACGTGGAG  
GCGCTGCGGCTGGCTGGCTGGGCTGAGCAGCTGGACGAGGGCTTCAAGCCGTTGCG  
AACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGCGCTGACGCCCTGCCCTGGAGCTGGGCTGAGCACACCCGATTGCCAGTGCAGGCC  
GAGGACCTGGCCGGCCTGGCTGCCCTGAGGAGCTGGATGTGAGCACCTAACCTGCG  
CCTGCCTGGCAGCTCTGGCCCTTCCCCGCTGCCCTGGGCTGTCAGCTGCCGCAACC  
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTGGCCCTGGGTGCGCAGAGCCACGTACA  
CTGGCCAGCCCTGAGGAGACGCCACTTGGCTGCCAGCCACCACAGCCACAGTGC  
GGAGCTTGA~~T~~ACTACGCCACTTGGCTGCCAGCCACCACAGCCACAGTGC  
CGAGGCCGTGGTGCAGGAGCCACAGCCTGTCTAGCTTGGCTCCTACCTGGCTTAGC  
CCCACAGGCCGGCACTGAGGCCCCAGCCGCCCTCACTGCCCAACCGACTGTAGGGCC  
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTAACGGGCAATGGGGCACATGCC  
GGACACGGCACCACCTGGCGTCTGTGCCCCGAAGGCTTACGGGCTGTACTGTGAGAGC  
CAGATGGGGCAGGGACACGCCAGCCCTACACCAGTCACGCCAGGCCACACGGTCC  
GACCTGGGATCGAGCCGGTGA~~G~~CCCCACCTCCCTGCCGTGGGCTGAGCCTACCTCC  
AGGGAGCTCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATGCC  
AAGCGGCTGGTGA~~G~~CCTGCAGCTGCAGCTGCCTGCCTCGCTGAGTACAGGT  
GCCAACGCCACTTACTCCGCTGTGTCATGCCCTGGGCCCCGGGGTGC  
AGGAGGCCTGCCGGGAGGCCATACACCCCAAGCCGCTCACTCCAACCACGCC  
CAGGCCGCAAGGGCAACCTGCCCTCATTGCCCGCCCTGCCCGGTGCTCTGG  
CGCGCTGGCTGCCGGTGGGGCAGCCTACTGTGCGGCCGGGGCATGGCAGCAGGG  
CTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCACTGAGGAGGCC  
CCCTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCC  
GTGTGAGGTGCCACTCATGGCTTCCAGGGCTGCCAGTCACCCCTCACGCAAAGC  
CCTACATT~~A~~AGCCAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCAACTCGGGATGTG  
CAGGGCTGTGACCACAGCTGGCCCTGTTCCCTGGA~~C~~CTCGGTCTCCTCATCTGTGAG  
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACGGAGTG  
CCGCCCTGCCCTCCGCAACGTGCA~~G~~TCCCTGGCAGGCCGGCCCTGCCATGTG  
GCATGCCCTGGCCCTGCTGGCTCTCCACTCCAGGGGCCACTGGGGCAGTGAAGGAAG  
CTCCCGAAAGAGCAGAGGGAGAGCAGGGTAGGCCGCTGTGACTCTAGT  
AAGCGAAGGAACAAAGAAACTGGAAAGGAGATGCTTAGGAACATG  
AATATATATATTATAAGAGATCCTTCCATTATTCTGGGAAGATG  
AGAGACAAGGACTTGGTTTGTAAGACAAACGATGATATGAAGGCC  
ATAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

-MW: 63030, PI: 7.24, NX(S/T): 3

<MW: 63030, PI: 7.21,  
MCSRVPLLLPLLLALGPVQGCPSCQCSQPQTVFCTARQTTVPRDVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLDLHSNSSLALEPGILDtanvealrl  
AGLGLQQLDEGLFSRLRNLDLSDNQLERVPPVIRGLRGLTRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWRESHVTLASP  
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGO  
GTRPSPTPVTPRPPRSLTGIEPVSPSLRVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLV  
TLRLPASLAETVTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQVGPAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

### Signal sequence.

## amino acids 1-23

#### Transmembrane domain.

amino acids 501-522

#### N-glycosylation sites:

amino acids 198-202, 425-429, 453-457  
as a kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites: amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

## amino acids 14-25

## EGF-like domain cysteine pattern signature.

amino acids 355-367

### Leucine zipper pattern.

amino acids 122-144, 194-216

## FIGURE 27

GGCACTAGGACAACCTTCTTCCCTCTGCACCCTGCCGTACCCCTACCCGCCACC  
TCCTTGCTACCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC**ATGCCAGCCTC**  
ATCTCCTTCTGCTAGCCCCAAAGGGCCTCCAGGAAACATGGGGGCCAGTCAGAGAGC  
CGGCACCTCAGTTGCCCTCTGGTTGAGTTGGGGGAGCTCTGGGGCGTGGCTGTGCC  
ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCTCCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAACAGCAGCACTCTGCACCTGGTTCCATTAAGCCACCTCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGAGAGGCCTAC  
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTATGCCAGGTC  
CTGTTCAAGACGTGACTTCAACATGGTCAGGTGGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCAGGCCTACAACAGCT  
GCTATAGCGAGGTGCTTCCATTACACCAAGGGATATTCTGAGTGTACATAATTCCCCGG  
GCAAGGGCGAAACTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACT**TGATT**  
GTGTTATAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGTACATACTGGAGACAGCAA  
GAGCTGAGTATATAAGGAGAGGAATGTGCAGGAACAGAGGCATCTTCCCTGGGTTGGCTC  
CCCGTTCTCACTTTCCCTTCATTCCCACCCCTAGACTTGATTACGGATATCTG  
CTTCTGTTCCCCATGGAGCTCCG

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	
DRAFTSMAN	

FIGURE 27

## FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722  
<subunit 1 of 1, 250 aa, 1 stop  
<MW: 27433, pI: 9.85, NX(S/T): 2  
MPASSPFLLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQLRREV  
SRLQGTGGPSQNNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN  
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFMGQVVSREG  
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFLGVKL

APPROVED	D.G. F.C.
CLASS	SUBCLASS
BY	
DRAFTSMAN	

**Signal sequence.**

amino acids 1-40

**N-glycosylation site.**

amino acids 124-128

**Tyrosine kinase phosphorylation site.**

amino acids 156-164

**N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

## **FIGURE 29**

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234  
><subunit 1 of 1, 281 aa, 1 stop  
><MW: 31743, pI: 6.83, NX(S/T): 1  
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP  
SQDQGLPASRCLRCCDPGTSMYPATAVQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH  
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFMFTGKFY  
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSOSLMLELREQDQVWV  
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

APPROVED	O.G. FIG.	SUBCLASS
	CLASS	
BY	DRAFTSMAN	

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

T07000 "20084446600

## FIGURE 31

APPROVED	O.G.	Fig.
BY	CLASS	SUBCLASS
DRAFTSMAN		

160  
150  
140  
130  
120  
110  
100  
90  
80  
70  
60  
50  
40  
30  
20  
10

GC GGAGCATCCGCTCGGGCCTCGCGAGACCCCGCGGGATTGCCGGTCTCCCGGG  
GCCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTCTAAAGCAAACATAAGACCAAGGGAGGATTAT  
CCTTGACCTTGAAGACAAAACACTAAACTGAAATTAAAATGTTCTCGGGGAGAAGGGAG  
CTTGACTTACACTTGGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC  
AGAGGCAATGAGCCC GTATATACTCAACTCAAGAAGACTGCATTAATTCTGCTGTTAAC  
AAAAAACATATCAGGGACAAAGCATGTAAC TTGATGATCTCGACACTCGAAAACAGCTA  
GACAACCCA ACTGCTACCTATTCTGCTCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTT GACCAGAAATTGCCAAG  
CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTCACAAGCAGTCACTCCCC  
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT  
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA  
GCTCCTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTACAATTTCCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
CATACCACCTCGGCTACTCCAAAGCCGCCACCCTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGACTTCCAGGCCACAGCTGGCCACCACAGCTCACCTGTAACCACACTGTCACCTCTC  
AGCCTCCCACGACCCTCATTCTACAGTTTACACGGCTGCCCTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATA CGTTACAGAAATCTCAA CTTAACACTTGAACACAGGGATGTGTATAACCCTA  
CTGCACTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCCCTCCAGGGAGTGTCCAGAAAATCAGTACGGCCTTCC  
ATTGAAAATGGCTCTTATCGGGTCCCTGCTTTGGTGTCTGTTCTGGTGTAGGCC  
TCGTCTCCTGGGTAGAATCCTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
TATTGATCAATGGATCTATGTGGACATCTAAGGATGGA ACTCGGTGTCTTAATTCTT  
TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTTGCTAGTCTAGCAGGAGGTTG  
TATTGAAAGACAGGAAAATGCCCTCTGCTTTCTTGTGAGACAGTCTCGGCTCTACCGCAACCTCGTCTC  
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTACCGCAACCTCGTCTC  
CTGGGTTCAAGCATTCTCCTGCCTCAGCCTCTAAGTATCTGGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTGTATT TAGAGAGACGGGTTTCACCATGTTGGTCAGGCTG  
GTCTCAAACCTCTGACCTAGTGATCCACCCCTCTCGGCCCTCCAAAGTGCTGGATTACAGG  
CATGAGCCACCACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAAATTGGGTAACTGTCTCTAAATATTGCTAAACAAAGCTCT  
ATGTAAAGTAATAAAAGTATAATTGCCATATAAAATTCAAAC TGCTTTATGCAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCACTTGGTTCCAGATAAAATCAAC  
TGTTATATCAATTCTAATGGATTGCTTTCTTTATATGGATTCCCTTAAACTTATT  
CCAGATGTAGTTCCATTAAATATTGAATAATCTTGTACTCAA

## FIGURE 32

FIG.	SUBCLASS
CLASS	
APPROVED BY	DRAFTSMAN

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCLKSLEDVVIDIQSSLKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLLETIPFTEISNLTNNTGNVYNPTALSMSNVESSTMNKTAWEGRREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYILINGIYVDI
```

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

## FIGURE 33

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

GCGGCACCTGGAAGATGCGCCATTGGCTGGTGGCCTGCTCAAGGTGGTTCGTGGCTTC  
GCCTCCTTGTGTGCCTGGTATTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAATGTGACCCTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAACAGTAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA  
ATGTGACAGCAACACGATGTTGATATGTATGAAGGCATAACTCTGGACCGATGACAAAG  
TTTATTCAAGAGTGCTGCTCCAAAATCCCTGCTCTCATGGTACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAACATGCCATAGAACGACTTGAAGTAAAGAAATCAGGAACA  
TGAAATTCAAGGTCTAGCTGGTATTGAGCAGCAAAAGGCTTGAACACTCCCTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAACAAACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGTACACTGCAGGGCCTGAGTAAAT  
GTGTTCTGTATAACAAATGCAGCTGGAAATCGCTCAAGAACATTATTTCTAAATCCAACA  
GCCCATTTGATGAGTATTTGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTATACCAAGTATTTATGAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTAAAAAAAAAA

100-12841-23341663

## FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777  
><subunit 1 of 1, 235 aa, 1 stop  
><MW: 25982, pI: 9.09, NX(S/T): 2  
MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMDYEGDNNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPABEQIEGCIPKERS

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125